SEQUENCE LISTING

<110> UNIVERSITÉ DE MONTRÉAL

<120> NEW METALLOPROTEASES OF THE NEPRILYSIN FAMILY

<130> BIOMEP INC. NEPRILYSIN

<140> PCT/CA/00/00147
<141> 2000-02-11

<150> 2,260,376
<151> 1999-02-11

<160> 17

<170> PatentIn Ver. 2.1

<210> 1
<211> 750
<212> PRT
<213> Homo sapiens

<400> 1

```
Met Gly Lys Ser Glu Ser Gln Met Asp Ile Thr Asp Ile Asn Thr Pro
  1               5                  10                  15

Lys Pro Lys Lys Lys Gln Arg Trp Thr Pro Leu Glu Ile Ser Leu Ser
             20                  25                  30

Val Leu Val Leu Leu Leu Thr Ile Ile Ala Val Thr Met Ile Ala Leu
         35                  40                  45

Tyr Ala Thr Tyr Asp Asp Gly Ile Cys Lys Ser Ser Asp Cys Ile Lys
     50                  55                  60

Ser Ala Ala Arg Leu Ile Gln Asn Met Asp Ala Thr Thr Glu Pro Cys
 65                  70                  75                  80

Thr Asp Phe Phe Lys Tyr Ala Cys Gly Gly Trp Leu Lys Arg Asn Val
                 85                  90                  95

Ile Pro Glu Thr Ser Ser Arg Tyr Gly Asn Phe Asp Ile Leu Arg Asp
            100                 105                 110

Glu Leu Glu Val Val Leu Lys Asp Val Leu Gln Glu Pro Lys Thr Glu
        115                 120                 125

Asp Ile Val Ala Val Gln Lys Ala Lys Ala Leu Tyr Arg Ser Cys Ile
    130                 135                 140

Asn Glu Ser Ala Ile Asp Ser Arg Gly Gly Glu Pro Leu Leu Lys Leu
145                 150                 155                 160

Leu Pro Asp Ile Tyr Gly Trp Pro Val Ala Thr Glu Asn Trp Glu Gln
                165                 170                 175
```

Lys Tyr Gly Ala Ser Trp Thr Ala Glu Lys Ala Ile Ala Gln Leu Asn
180 185 190

Ser Lys Tyr Gly Lys Lys Val Leu Ile Asn Leu Phe Val Gly Thr Asp
195 200 205

Asp Lys Asn Ser Val Asn His Val Ile His Ile Asp Gln Pro Arg Leu
210 215 220

Gly Leu Pro Ser Arg Asp Tyr Tyr Glu Cys Thr Gly Ile Tyr Lys Glu
225 230 235 240

Ala Cys Thr Ala Tyr Val Asp Phe Met Ile Ser Val Ala Arg Leu Ile
245 250 255

Arg Gln Glu Glu Arg Leu Pro Ile Asp Glu Asn Gln Leu Ala Leu Glu
260 265 270

Met Asn Lys Val Met Glu Leu Glu Lys Glu Ile Ala Asn Ala Thr Ala
275 280 285

Lys Pro Glu Asp Arg Asn Asp Pro Met Leu Leu Tyr Asn Lys Met Thr
290 295 300

Leu Ala Gln Ile Gln Asn Asn Phe Ser Leu Glu Ile Asn Gly Lys Pro
305 310 315 320

Phe Ser Trp Leu Asn Phe Thr Asn Glu Ile Met Ser Thr Val Asn Ile
325 330 335

Ser Ile Thr Asn Glu Glu Asp Val Val Val Tyr Ala Pro Glu Tyr Leu
340 345 350

Thr Lys Leu Lys Pro Ile Leu Thr Lys Tyr Ser Ala Arg Asp Leu Gln
355 360 365

Asn Leu Met Ser Trp Arg Phe Ile Met Asp Leu Val Ser Ser Leu Ser
370 375 380

Arg Thr Tyr Lys Glu Ser Arg Asn Ala Phe Arg Lys Ala Leu Tyr Gly
385 390 395 400

Thr Thr Ser Glu Thr Ala Thr Trp Arg Arg Cys Ala Asn Tyr Val Asn
405 410 415

Gly Asn Met Glu Asn Ala Val Gly Arg Leu Tyr Val Glu Ala Ala Phe
420 425 430

Ala Gly Glu Ser Lys His Val Val Glu Asp Leu Ile Ala Gln Ile Arg
435 440 445

Glu Val Phe Ile Gln Thr Leu Asp Asp Leu Thr Trp Met Asp Ala Glu
450 455 460

Thr Lys Lys Arg Ala Glu Glu Lys Ala Leu Ala Ile Lys Glu Arg Ile
465 470 475 480

```
Gly Tyr Pro Asp Asp Ile Val Ser Asn Asp Asn Lys Leu Asn Asn Glu
                485                 490                 495

Tyr Leu Glu Leu Asn Tyr Lys Glu Asp Glu Tyr Phe Glu Asn Ile Ile
            500                 505                 510

Gln Asn Leu Lys Phe Ser Gln Ser Lys Gln Leu Lys Lys Leu Arg Glu
        515                 520                 525

Lys Val Asp Lys Asp Glu Trp Ile Ser Gly Ala Ala Val Val Asn Ala
    530                 535                 540

Phe Tyr Ser Ser Gly Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu
545                 550                 555                 560

Gln Pro Pro Phe Phe Ser Ala Gln Gln Ser Asn Ser Leu Asn Tyr Gly
                565                 570                 575

Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp
            580                 585                 590

Asn Gly Arg Asn Phe Asn Lys Asp Gly Asp Leu Val Asp Trp Trp Thr
        595                 600                 605

Gln Gln Ser Ala Ser Asn Phe Lys Glu Gln Ser Gln Cys Met Val Tyr
    610                 615                 620

Gln Tyr Gly Asn Phe Ser Trp Asp Leu Ala Gly Gly Gln His Leu Asn
625                 630                 635                 640

Gly Ile Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Gly
                645                 650                 655

Gln Ala Tyr Arg Ala Tyr Gln Asn Tyr Ile Lys Lys Asn Gly Glu Glu
            660                 665                 670

Lys Leu Leu Pro Gly Leu Asp Leu Asn His Lys Gln Leu Phe Phe Leu
        675                 680                 685

Asn Phe Ala Gln Val Trp Cys Gly Thr Tyr Arg Pro Glu Tyr Ala Val
    690                 695                 700

Asn Ser Ile Lys Thr Asp Val His Ser Pro Gly Asn Phe Arg Ile Ile
705                 710                 715                 720

Gly Thr Leu Gln Asn Ser Ala Glu Phe Ser Glu Ala Phe His Cys Arg
                725                 730                 735

Lys Asn Ser Tyr Met Asn Pro Glu Lys Lys Cys Arg Val Trp
            740                 745                 750
```

<210> 2
<211> 749
<212> PRT
<213> Homo sapiens

<400> 2

```
Met Glu Ala Glu Thr Gly Ser Ser Val Glu Thr Gly Lys Lys Ala Asn
  1               5                  10                  15

Arg Gly Thr Arg Ile Ala Leu Val Val Phe Val Gly Gly Thr Leu Val
             20                  25                  30

Leu Gly Thr Ile Leu Phe Leu Val Ser Gln Gly Leu Leu Ser Leu Gln
         35                  40                  45

Ala Lys Gln Glu Tyr Cys Leu Lys Pro Glu Cys Ile Glu Ala Ala Ala
     50                  55                  60

Ala Ile Leu Ser Lys Val Asn Leu Ser Val Asp Pro Cys Asp Asn Phe
 65                  70                  75                  80

Phe Arg Phe Ala Cys Asp Gly Trp Ile Ser Asn Asn Pro Ile Pro Glu
                 85                  90                  95

Asp Met Pro Ser Tyr Gly Val Tyr Pro Trp Leu Arg His Asn Val Asp
            100                 105                 110

Leu Lys Leu Lys Glu Leu Leu Glu Lys Ser Ile Ser Arg Arg Arg Asp
        115                 120                 125

Thr Glu Ala Ile Gln Lys Ala Lys Ile Leu Tyr Ser Ser Cys Met Asn
    130                 135                 140

Glu Lys Ala Ile Glu Lys Ala Asp Ala Lys Pro Leu Leu His Ile Leu
145                 150                 155                 160

Arg His Ser Pro Phe Arg Trp Pro Val Leu Glu Ser Asn Ile Gly Pro
                165                 170                 175

Glu Gly Val Trp Ser Glu Arg Lys Phe Ser Leu Leu Gln Thr Leu Ala
            180                 185                 190

Thr Phe Arg Gly Gln Tyr Ser Asn Ser Val Phe Ile Arg Leu Tyr Val
        195                 200                 205

Ser Pro Asp Asp Lys Ala Ser Asn Glu His Ile Leu Lys Leu Asp Gln
    210                 215                 220

Ala Thr Leu Ser Leu Ala Val Arg Glu Asp Tyr Leu Asp Asn Ser Thr
225                 230                 235                 240

Glu Ala Lys Ser Tyr Arg Asp Ala Leu Tyr Lys Phe Met Val Asp Thr
                245                 250                 255

Ala Val Leu Leu Gly Ala Asn Ser Ser Arg Ala Glu His Asp Met Lys
            260                 265                 270

Ser Val Leu Arg Leu Glu Ile Lys Ile Ala Glu Ile Met Ile Pro His
        275                 280                 285

Glu Asn Arg Thr Ser Glu Ala Met Tyr Asn Lys Met Asn Ile Ser Glu
    290                 295                 300
```

Leu Ser Ala Met Ile Pro Gln Phe Asp Trp Leu Gly Tyr Ile Lys Lys
305 310 315 320

Val Ile Asp Thr Arg Leu Tyr Pro His Leu Lys Asp Ile Ser Pro Ser
325 330 335

Glu Asn Val Val Val Arg Val Pro Gln Tyr Phe Lys Asp Leu Phe Arg
340 345 350

Ile Leu Gly Ser Glu Arg Lys Lys Thr Ile Ala Asn Tyr Leu Val Trp
355 360 365

Arg Met Val Tyr Ser Arg Ile Pro Asn Leu Ser Arg Arg Phe Gln Tyr
370 375 380

Arg Trp Leu Glu Phe Ser Arg Val Ile Gln Gly Thr Thr Thr Leu Leu
385 390 395 400

Pro Gln Trp Asp Lys Cys Val Asn Phe Ile Glu Ser Ala Leu Pro Tyr
405 410 415

Val Val Gly Lys Met Phe Val Asp Val Tyr Phe Gln Glu Asp Lys Lys
420 425 430

Glu Met Met Glu Glu Leu Val Glu Gly Val Arg Trp Ala Phe Ile Asp
435 440 445

Met Leu Glu Lys Glu Asn Glu Trp Met Asp Ala Gly Thr Lys Arg Lys
450 455 460

Ala Lys Glu Lys Ala Arg Ala Val Leu Ala Lys Val Gly Tyr Pro Glu
465 470 475 480

Phe Ile Met Asn Asp Thr His Val Asn Glu Asp Leu Lys Ala Ile Lys
485 490 495

Phe Ser Glu Ala Asp Tyr Phe Gly Asn Val Leu Gln Thr Arg Lys Tyr
500 505 510

Leu Ala Gln Ser Asp Phe Phe Trp Leu Arg Lys Ala Val Pro Lys Thr
515 520 525

Glu Trp Phe Thr Asn Pro Thr Thr Val Asn Ala Phe Tyr Ser Ala Ser
530 535 540

Thr Asn Gln Ile Arg Phe Pro Ala Gly Glu Leu Gln Lys Pro Phe Phe
545 550 555 560

Trp Gly Thr Glu Tyr Pro Arg Ser Leu Ser Tyr Gly Ala Ile Gly Val
565 570 575

Ile Val Gly His Glu Phe Thr His Gly Phe Asp Asn Asn Gly Arg Lys
580 585 590

Tyr Asp Lys Asn Gly Asn Leu Asp Pro Trp Trp Ser Thr Glu Ser Glu
595 600 605

```
Glu Lys Phe Lys Glu Lys Thr Lys Cys Met Ile Asn Gln Tyr Ser Asn
    610                 615                 620

Tyr Tyr Trp Lys Lys Ala Gly Leu Asn Val Lys Gly Lys Arg Thr Leu
625                 630                 635                 640

Gly Glu Asn Ile Ala Asp Asn Gly Gly Leu Arg Glu Ala Phe Arg Ala
                645                 650                 655

Tyr Arg Lys Trp Ile Asn Asp Arg Arg Gln Gly Leu Glu Glu Pro Leu
            660                 665                 670

Leu Pro Gly Ile Thr Phe Thr Asn Asn Gln Leu Phe Phe Leu Ser Tyr
        675                 680                 685

Ala His Val Arg Cys Asn Ser Tyr Arg Pro Glu Ala Ala Arg Glu Gln
    690                 695                 700

Val Gln Ile Gly Ala His Ser Pro Pro Gln Phe Arg Val Asn Gly Ala
705                 710                 715                 720

Ile Ser Asn Phe Glu Glu Phe Gln Lys Ala Phe Asn Cys Pro Pro Asn
                725                 730                 735

Ser Thr Met Asn Arg Gly Met Asp Ser Cys Arg Leu Trp
            740                 745


<210> 3
<211> 732
<212> PRT
<213> Homo sapiens

<400> 3
Met Glu Gly Gly Asp Gln Ser Glu Glu Glu Pro Arg Glu Arg Ser Gln
  1               5                  10                  15

Ala Gly Gly Met Gly Thr Leu Trp Ser Gln Glu Ser Thr Pro Glu Glu
            20                  25                  30

Arg Leu Pro Val Glu Gly Ser Arg Pro Trp Ala Val Ala Arg Arg Val
        35                  40                  45

Leu Thr Ala Ile Leu Ile Leu Gly Leu Leu Leu Cys Phe Ser Val Leu
    50                  55                  60

Leu Phe Tyr Asn Phe Gln Asn Cys Gly Pro Arg Pro Cys Glu Thr Ser
65                  70                  75                  80

Val Cys Leu Asp Leu Arg Asp His Tyr Leu Ala Ser Gly Asn Thr Ser
                85                  90                  95

Val Ala Pro Cys Thr Asp Phe Phe Ser Phe Ala Cys Gly Arg Ala Lys
            100                 105                 110

Glu Thr Asn Asn Ser Phe Gln Glu Leu Ala Thr Lys Asn Lys Asn Arg
```

```
        115                 120                 125

Leu Arg Arg Ile Leu Glu Val Gln Asn Ser Trp His Pro Gly Ser Gly
    130                 135                 140

Glu Glu Lys Ala Phe Gln Phe Tyr Asn Ser Cys Met Asp Thr Leu Ala
145                 150                 155                 160

Ile Glu Ala Ala Gly Thr Gly Pro Leu Arg Gln Val Ile Glu Glu Leu
                165                 170                 175

Gly Gly Trp Arg Ile Ser Gly Lys Trp Thr Ser Leu Asn Phe Asn Arg
            180                 185                 190

Thr Leu Arg Leu Leu Met Ser Gln Tyr Gly His Phe Pro Phe Phe Arg
        195                 200                 205

Ala Tyr Leu Gly Pro His Pro Ala Ser Pro His Thr Pro Val Ile Gln
    210                 215                 220

Ile Asp Gln Pro Glu Phe Asp Val Pro Leu Lys Gln Asp Gln Glu Gln
225                 230                 235                 240

Lys Ile Tyr Ala Gln Ile Phe Arg Glu Tyr Leu Thr Tyr Leu Asn Gln
                245                 250                 255

Leu Gly Thr Leu Leu Gly Gly Asp Pro Ser Lys Val Gln Glu His Ser
            260                 265                 270

Ser Leu Ser Ile Ser Ile Thr Ser Arg Leu Phe Gln Phe Leu Arg Pro
        275                 280                 285

Leu Glu Gln Arg Arg Ala Gln Gly Lys Leu Phe Gln Met Val Thr Ile
    290                 295                 300

Asp Gln Leu Lys Glu Met Ala Pro Ala Ile Asp Trp Leu Ser Cys Leu
305                 310                 315                 320

Gln Ala Thr Phe Thr Pro Met Ser Leu Ser Pro Ser Gln Ser Leu Val
                325                 330                 335

Val His Asp Val Glu Tyr Leu Lys Asn Met Ser Gln Leu Val Glu Glu
            340                 345                 350

Met Leu Leu Lys Gln Arg Asp Phe Leu Gln Ser His Met Ile Leu Gly
        355                 360                 365

Leu Val Val Thr Leu Ser Pro Ala Leu Asp Ser Gln Phe Gln Glu Ala
    370                 375                 380

Arg Arg Lys Leu Ser Gln Lys Leu Arg Glu Leu Thr Glu Gln Pro Pro
385                 390                 395                 400

Met Pro Ala Arg Pro Arg Trp Met Lys Cys Val Glu Glu Thr Gly Thr
                405                 410                 415

Phe Phe Glu Pro Thr Leu Ala Ala Leu Phe Val Arg Glu Ala Phe Gly
```

```
            420                 425                 430

Pro Ser Thr Arg Ser Ala Ala Met Lys Leu Phe Thr Ala Ile Arg Asp
        435                 440                 445

Ala Leu Ile Thr Arg Leu Arg Asn Leu Pro Trp Met Asn Glu Glu Thr
    450                 455                 460

Gln Asn Met Ala Gln Asp Lys Val Ala Gln Leu Gln Val Glu Met Gly
465                 470                 475                 480

Ala Ser Glu Trp Ala Leu Lys Pro Glu Leu Ala Arg Gln Glu Tyr Asn
                485                 490                 495

Asp Ile Gln Leu Gly Ser Ser Phe Leu Gln Ser Val Leu Ser Cys Val
            500                 505                 510

Arg Ser Leu Arg Ala Arg Ile Val Gln Ser Phe Leu Gln Pro His Pro
        515                 520                 525

Gln His Arg Trp Lys Val Ser Pro Trp Asp Val Asn Ala Tyr Tyr Ser
    530                 535                 540

Val Ser Asp His Val Val Val Phe Pro Ala Gly Leu Leu Gln Pro Pro
545                 550                 555                 560

Phe Phe His Pro Gly Tyr Pro Arg Ala Val Asn Phe Gly Ala Ala Gly
                565                 570                 575

Ser Ile Met Ala His Glu Leu Leu His Ile Phe Tyr Gln Leu Leu Leu
            580                 585                 590

Pro Gly Gly Cys Leu Ala Cys Asp Asn His Ala Leu Gln Glu Ala His
        595                 600                 605

Leu Cys Leu Lys Arg His Tyr Ala Ala Phe Pro Leu Pro Ser Arg Thr
    610                 615                 620

Ser Phe Asn Asp Ser Leu Thr Phe Leu Glu Asn Ala Ala Asp Val Gly
625                 630                 635                 640

Gly Leu Ala Ile Ala Leu Gln Ala Tyr Ser Lys Arg Leu Leu Arg His
                645                 650                 655

His Gly Glu Thr Val Leu Pro Ser Leu Asp Leu Ser Pro Gln Gln Ile
            660                 665                 670

Phe Phe Arg Ser Tyr Ala Gln Val Met Cys Arg Lys Pro Ser Pro Gln
        675                 680                 685

Asp Ser His Asp Thr His Ser Pro Pro His Leu Arg Val His Gly Pro
    690                 695                 700

Leu Ser Ser Thr Pro Ala Phe Ala Arg Tyr Phe Arg Cys Ala Arg Gly
705                 710                 715                 720

Ala Leu Leu Asn Pro Ser Ser Arg Cys Gln Leu Trp
```

<210> 4
<211> 753
<212> PRT
<213> Homo sapiens

<400> 4

```
Met Ser Thr Tyr Lys Arg Ala Thr Leu Asp Glu Glu Asp Leu Val Asp
  1               5                  10                  15

Ser Leu Ser Glu Gly Asp Ala Tyr Pro Asn Gly Leu Gln Val Asn Phe
             20                  25                  30

His Ser Pro Arg Ser Gly Gln Arg Cys Trp Ala Ala Arg Thr Gln Val
         35                  40                  45

Glu Lys Arg Leu Val Val Leu Val Val Leu Leu Ala Ala Gly Leu Val
     50                  55                  60

Ala Cys Leu Ala Ala Leu Gly Ile Gln Tyr Gln Thr Arg Ser Pro Ser
 65                  70                  75                  80

Val Cys Leu Ser Glu Ala Cys Val Ser Val Thr Ser Ser Ile Leu Ser
                 85                  90                  95

Ser Met Asp Pro Thr Val Asp Pro Cys His Asp Phe Phe Ser Tyr Ala
            100                 105                 110

Cys Gly Gly Trp Ile Lys Ala Asn Pro Val Pro Asp Gly His Ser Arg
        115                 120                 125

Trp Gly Thr Phe Ser Asn Leu Trp Glu His Asn Gln Ala Ile Ile Lys
    130                 135                 140

His Leu Leu Glu Asn Ser Thr Ala Ser Val Ser Glu Ala Glu Arg Lys
145                 150                 155                 160

Ala Gln Val Tyr Tyr Arg Ala Cys Met Asn Glu Thr Arg Ile Glu Glu
                165                 170                 175

Leu Arg Ala Lys Pro Leu Met Glu Leu Ile Glu Arg Leu Gly Gly Trp
            180                 185                 190

Asn Ile Thr Gly Pro Trp Ala Lys Asp Asn Phe Gln Asp Thr Leu Gln
        195                 200                 205

Val Val Thr Ala His Tyr Arg Thr Ser Pro Phe Phe Ser Val Tyr Val
    210                 215                 220

Ser Ala Asp Ser Lys Asn Ser Asn Ser Asn Val Ile Gln Val Asp Gln
225                 230                 235                 240

Ser Gly Leu Gly Leu Pro Ser Arg Asp Tyr Tyr Leu Asn Lys Thr Glu
                245                 250                 255
```

```
Asn Glu Lys Val Leu Thr Gly Tyr Leu Asn Tyr Met Val Gln Leu Gly
            260                 265                 270

Lys Leu Leu Gly Gly Gly Asp Glu Glu Ala Ile Arg Pro Gln Met Gln
        275                 280                 285

Gln Ile Leu Asp Phe Glu Thr Ala Leu Ala Asn Ile Thr Ile Pro Gln
    290                 295                 300

Glu Lys Arg Arg Asp Glu Glu Leu Ile Tyr His Lys Val Thr Ala Ala
305                 310                 315                 320

Glu Leu Gln Thr Leu Ala Pro Ala Ile Asn Trp Leu Pro Phe Leu Asn
                325                 330                 335

Thr Ile Phe Tyr Pro Val Glu Ile Asn Glu Ser Glu Pro Ile Val Val
            340                 345                 350

Tyr Asp Lys Glu Tyr Leu Glu Gln Ile Ser Thr Leu Ile Asn Thr Thr
        355                 360                 365

Asp Arg Cys Leu Leu Asn Asn Tyr Met Ile Trp Asn Leu Val Arg Lys
    370                 375                 380

Thr Ser Ser Phe Leu Asp Gln Arg Phe Gln Asp Ala Asp Glu Lys Phe
385                 390                 395                 400

Met Glu Val Met Tyr Gly Thr Lys Lys Thr Cys Leu Pro Arg Trp Lys
                405                 410                 415

Phe Cys Val Ser Asp Thr Glu Asn Asn Leu Gly Phe Ala Leu Gly Pro
            420                 425                 430

Met Phe Val Lys Ala Thr Phe Ala Glu Asp Ser Lys Ser Ile Ala Thr
        435                 440                 445

Glu Ile Ile Leu Glu Ile Lys Lys Ala Phe Glu Glu Ser Leu Ser Thr
    450                 455                 460

Leu Lys Trp Met Asp Glu Glu Thr Arg Lys Ser Ala Lys Glu Lys Ala
465                 470                 475                 480

Asp Ala Ile Tyr Asn Met Ile Gly Tyr Pro Asn Phe Ile Met Asp Pro
                485                 490                 495

Lys Glu Leu Asp Lys Val Phe Asn Asp Tyr Thr Ala Val Pro Asp Leu
            500                 505                 510

Tyr Phe Glu Asn Ala Met Arg Phe Phe Asn Phe Ser Trp Arg Val Thr
        515                 520                 525

Ala Asp Gln Leu Arg Lys Ala Pro Asn Arg Asp Gln Trp Ser Met Thr
    530                 535                 540

Pro Pro Met Val Asn Ala Tyr Tyr Ser Pro Thr Lys Asn Glu Ile Val
545                 550                 555                 560
```

```
Phe Pro Ala Gly Ile Leu Gln Ala Pro Phe Tyr Thr Arg Ser Ser Pro
                565                 570                 575

Lys Ala Leu Asn Phe Gly Gly Ile Gly Val Val Val Gly His Glu Leu
            580                 585                 590

Thr His Ala Phe Asp Asp Gln Gly Arg Glu Tyr Asp Lys Asp Gly Asn
        595                 600                 605

Leu Arg Pro Trp Trp Lys Asn Ser Ser Val Glu Ala Phe Lys Arg Gln
    610                 615                 620

Thr Glu Cys Met Val Glu Gln Tyr Ser Asn Tyr Ser Val Asn Gly Glu
625                 630                 635                 640

Pro Val Asn Gly Arg His Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly
                645                 650                 655

Gly Leu Lys Ala Ala Tyr Arg Ala Tyr Gln Asn Trp Val Lys Lys Asn
            660                 665                 670

Gly Ala Glu His Ser Leu Pro Thr Leu Gly Leu Thr Asn Asn Gln Leu
        675                 680                 685

Phe Phe Leu Gly Phe Ala Gln Val Trp Cys Ser Val Arg Thr Pro Glu
    690                 695                 700

Ser Ser His Glu Gly Leu Ile Thr Asp Pro His Ser Pro Ser Arg Phe
705                 710                 715                 720

Arg Val Ile Gly Ser Leu Ser Asn Ser Lys Glu Phe Ser Glu His Phe
                725                 730                 735

Arg Cys Pro Pro Gly Ser Pro Met Asn Pro Pro His Lys Cys Glu Val
            740                 745                 750

Trp
```

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (14)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base

<222> (21)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<400> 5
tggatggatc gacngganac naca 24

<210> 6
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (14)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base
<222> (21)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<400> 6
tggatggatc gacngganac nacg 24

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (4)
<223> i

<220>
<221> modified_base
<222> (7)
<223> i

<220>
<221> modified_base
<222> (14)

<223> i

<220>
<221> modified_base
<222> (17)
<223> i

<220>
<221> modified_base
<222> (20)
<223> i

<220>
<221> modified_base
<222> (25)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<400> 7
agtngtnttt cccngcnggn agtancttat ca 32

<210> 8
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (4)
<223> i

<220>
<221> modified_base
<222> (7)
<223> i

<220>
<221> modified_base
<222> (14)
<223> i

<220>
<221> modified_base
<222> (17)
<223> i

<220>
<221> modified_base
<222> (20)
<223> i

<220>
<221> modified_base

<222> (25)
<223> i

<220>
<223> Description of Artificial Sequence:
Oligonucleotide primers for RT-PCR reactions

<400> 8
agtngtnttt cccngcnggn agtancttgc ca 32

<210> 9
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (2)
<223> i

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<220>
<221> modified_base
<222> (21)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<220>
<221> modified_base
<222> (3)
<223> i

<400> 9
annccnccna tctagtcngc ngactagttt ctc 33

<210> 10
<211> 35
<212> DNA

<213> Artificial Sequence

<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> modified_base
<222> (24)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<400> 10
gatcaatctc tngatcgaag tctnaatctg gatgg 35

<210> 11
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<220>
<221> modified_base
<222> (31)
<223> i

<220>
<223> Description of Artificial Sequence:Oligonucleotide
primers for RT-PCR reactions

<400> 11
tctcaccana tnctgagcat cgttcttcat ngggatg 37

<210> 12
<211> 2925
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (332)..(2626)

<400> 12
cgggagccag caccgtgtga cctcacaccc agctcagctg ctctactcca cccggagccc 60

accttggcca gctcacccca actctgagac atcccaacct agcctttaag gacttgccta 120

gcagtgactg agagcaccag ggtcccctgg gcacttgggg cacagcttac agcattgaga 180

gcagagacca ggacagtgca ccagcttcag tgtgtcctag gcatccgatc cgggctccag 240

ctgcctctct cctagccctg gcctgggggg cttagcggtg tgccttccac ccagaaccgg 300

ctgataggga aagtctgaga gcccagtggg g atg gtg gag aga gca ggc tgg 352
Met Val Glu Arg Ala Gly Trp
1 5

tgt cgg aag aag tcc cca ggc ttc gtg gag tat ggg ctg atg gtg ctg 400
Cys Arg Lys Lys Ser Pro Gly Phe Val Glu Tyr Gly Leu Met Val Leu
10 15 20

ctg ctg ctg ttg ctg gga gcc ata gtg act ctg ggt gtc ttc tac agc 448
Leu Leu Leu Leu Leu Gly Ala Ile Val Thr Leu Gly Val Phe Tyr Ser
25 30 35

ata ggg aag cag ctg ccc ctc tta act agc ctg cta cac ttc tcc tgg 496
Ile Gly Lys Gln Leu Pro Leu Leu Thr Ser Leu Leu His Phe Ser Trp
40 45 50 55

gat gag agg acg gtt gta aaa cga gcc ctc agg gat tca tca ctg aaa 544
Asp Glu Arg Thr Val Val Lys Arg Ala Leu Arg Asp Ser Ser Leu Lys
60 65 70

agt gac atc tgc acc acc cca agc tgt gtg ata gca gct gcc aga atc 592
Ser Asp Ile Cys Thr Thr Pro Ser Cys Val Ile Ala Ala Ala Arg Ile
75 80 85

ctc gaa aac atg gac caa tcg agg aac ccc tgt gaa aac ttc tac cag 640
Leu Glu Asn Met Asp Gln Ser Arg Asn Pro Cys Glu Asn Phe Tyr Gln
90 95 100

tac gcc tgc gga ggc tgg ctg agg cac cac gtg atc cca gag acc aac 688
Tyr Ala Cys Gly Gly Trp Leu Arg His His Val Ile Pro Glu Thr Asn
105 110 115

tcc cga tac agc gtc ttt gac atc ctg cgg gac gag ctg gag gtt atc 736
Ser Arg Tyr Ser Val Phe Asp Ile Leu Arg Asp Glu Leu Glu Val Ile
120 125 130 135

ctc aaa ggg gtg ctg gag gat tcc act tcc cag cat cgc ccg gcc gtg 784
Leu Lys Gly Val Leu Glu Asp Ser Thr Ser Gln His Arg Pro Ala Val
140 145 150

gag aag gcc aag aca cta tat cgc tcc tgc atg aac caa agt gtg atc 832
Glu Lys Ala Lys Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile
155 160 165

gag aag aga gac tct gag ccc ctg ctg agc gtc tta aaa atg gta gga 880
Glu Lys Arg Asp Ser Glu Pro Leu Leu Ser Val Leu Lys Met Val Gly

```
        170                 175                 180

ggt tgg cct gtg gcc atg gat aag tgg aac gag acc atg ggc ctc aag   928
Gly Trp Pro Val Ala Met Asp Lys Trp Asn Glu Thr Met Gly Leu Lys
    185                 190                 195

tgg gaa ctg gag cga cag ttg gct gtg ttg aac tcg cag ttc aac agg   976
Trp Glu Leu Glu Arg Gln Leu Ala Val Leu Asn Ser Gln Phe Asn Arg
200                 205                 210                 215

cgg gtc ctc atc gac ctc ttc atc tgg aat gac gac cag aac tcc agc   1024
Arg Val Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser
                220                 225                 230

cgg cat gtc atc tac ata gac cag ccc acc ttg ggc atg cca tcc cgg   1072
Arg His Val Ile Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg
            235                 240                 245

gag tac tat ttc cag gag gac aac aac cac aag gta cgg aaa gcc tac   1120
Glu Tyr Tyr Phe Gln Glu Asp Asn Asn His Lys Val Arg Lys Ala Tyr
        250                 255                 260

ctg gag ttc atg acg tca gtg gcc act atg ctt agg aaa gac cag aac   1168
Leu Glu Phe Met Thr Ser Val Ala Thr Met Leu Arg Lys Asp Gln Asn
    265                 270                 275

ctg tcc aag gag agc gcc atg gtg cgg gag gag atg gcg gag gtg ctg   1216
Leu Ser Lys Glu Ser Ala Met Val Arg Glu Glu Met Ala Glu Val Leu
280                 285                 290                 295

gaa ctg gag acg cat ctg gcc aac gcc aca gtc ccc cag gag aaa agg   1264
Glu Leu Glu Thr His Leu Ala Asn Ala Thr Val Pro Gln Glu Lys Arg
                300                 305                 310

cat gat gtc act gcc ctg tac cac cga atg gac ctg atg gag cta cag   1312
His Asp Val Thr Ala Leu Tyr His Arg Met Asp Leu Met Glu Leu Gln
            315                 320                 325

gaa agg ttt ggt ctg aag ggg ttt aac tgg act ctc ttc ata caa aac   1360
Glu Arg Phe Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Asn
        330                 335                 340

gtg ttg tct tct gtg gaa gtc gag ctg ttc cca gat gag gag gtg gtg   1408
Val Leu Ser Ser Val Glu Val Glu Leu Phe Pro Asp Glu Glu Val Val
    345                 350                 355

gtc tac ggc atc ccc tac ctg gag aat ctg gag gat atc att gat agc   1456
Val Tyr Gly Ile Pro Tyr Leu Glu Asn Leu Glu Asp Ile Ile Asp Ser
360                 365                 370                 375

tac tca gca cgg acc atg cag aac tac ctg gta tgg cgc ctg gtg cta   1504
Tyr Ser Ala Arg Thr Met Gln Asn Tyr Leu Val Trp Arg Leu Val Leu
                380                 385                 390

gat cga att ggc agc ctg agc cag aga ttc aaa gag gcg cgt gtg gac   1552
Asp Arg Ile Gly Ser Leu Ser Gln Arg Phe Lys Glu Ala Arg Val Asp
            395                 400                 405
```

```
tac cgc aag gcg ctg tac ggc acg acc gtg gag gag gta cgc tgg cga   1600
Tyr Arg Lys Ala Leu Tyr Gly Thr Thr Val Glu Glu Val Arg Trp Arg
        410                 415                 420

gag tgt gtc agc tat gtc aac agt aac atg gag agc gcc gtg ggc tcc   1648
Glu Cys Val Ser Tyr Val Asn Ser Asn Met Glu Ser Ala Val Gly Ser
    425                 430                 435

ctc tac atc aag cgg gcc ttc tcc aag gac agc aag agc acg gtc aga   1696
Leu Tyr Ile Lys Arg Ala Phe Ser Lys Asp Ser Lys Ser Thr Val Arg
440                 445                 450                 455

gag ctg att gag aag ata agg tcc gtg ttt gtg gat aac ctg gat gag   1744
Glu Leu Ile Glu Lys Ile Arg Ser Val Phe Val Asp Asn Leu Asp Glu
                460                 465                 470

ctg aac tgg atg gac gag gaa tcc aag aag aag gcc cag gaa aag gcc   1792
Leu Asn Trp Met Asp Glu Glu Ser Lys Lys Lys Ala Gln Glu Lys Ala
            475                 480                 485

atg aat ata cgg gaa cag att ggc tac cct gac tac att ttg gaa gat   1840
Met Asn Ile Arg Glu Gln Ile Gly Tyr Pro Asp Tyr Ile Leu Glu Asp
        490                 495                 500

aac aat aaa cac ctg gat gag gaa tac tcc agt ttg act ttc tat gag   1888
Asn Asn Lys His Leu Asp Glu Glu Tyr Ser Ser Leu Thr Phe Tyr Glu
    505                 510                 515

gac ctg tat ttt gag aac gga ctt cag aac ctc aag aac aat gcc cag   1936
Asp Leu Tyr Phe Glu Asn Gly Leu Gln Asn Leu Lys Asn Asn Ala Gln
520                 525                 530                 535

agg agc ctc aag aag ctt cgg gaa aag gtg gac cag aat ctc tgg atc   1984
Arg Ser Leu Lys Lys Leu Arg Glu Lys Val Asp Gln Asn Leu Trp Ile
                540                 545                 550

atc ggg gct gca gtg gtc aat gca ttc tac tcc cca aac aga aac cag   2032
Ile Gly Ala Ala Val Val Asn Ala Phe Tyr Ser Pro Asn Arg Asn Gln
            555                 560                 565

atc gtc ttt cca gca ggg att ctc cag ccg ccc ttc ttc agc aag gac   2080
Ile Val Phe Pro Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Lys Asp
        570                 575                 580

caa cca cag tcc ttg aat ttt ggg ggc atc ggg atg gtg att ggg cac   2128
Gln Pro Gln Ser Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His
    585                 590                 595

gag atc aca cac ggc ttt gat gat aat ggt cgt aac ttt gac aag aac   2176
Glu Ile Thr His Gly Phe Asp Asp Asn Gly Arg Asn Phe Asp Lys Asn
600                 605                 610                 615

ggc aac atg ctg gac tgg tgg agt aac ttc tcg gcc cgg cac ttc caa   2224
Gly Asn Met Leu Asp Trp Trp Ser Asn Phe Ser Ala Arg His Phe Gln
                620                 625                 630
```

```
cag cag tcg caa tgc atg atc tat cag tac ggc aac ttc tct tgg gaa   2272
Gln Gln Ser Gln Cys Met Ile Tyr Gln Tyr Gly Asn Phe Ser Trp Glu
            635                 640                 645

cta gca gac aac cag aat gtg aac gga ttc agt acc ctc ggg gag aac   2320
Leu Ala Asp Asn Gln Asn Val Asn Gly Phe Ser Thr Leu Gly Glu Asn
        650                 655                 660

att gcc gac aac gga ggt gtg cga cag gca tac aag gct tac cta cgg   2368
Ile Ala Asp Asn Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Arg
    665                 670                 675

tgg ctg gct gat ggc ggc aaa gat cag cga ctg ccg gga ctg aac ctg   2416
Trp Leu Ala Asp Gly Gly Lys Asp Gln Arg Leu Pro Gly Leu Asn Leu
680                 685                 690                 695

acc tat gcc cag ctt ttc ttc atc aac tat gcc cag gtg tgg tgt ggg   2464
Thr Tyr Ala Gln Leu Phe Phe Ile Asn Tyr Ala Gln Val Trp Cys Gly
                700                 705                 710

tcc tat agg ccg gag ttc gcc gtc cag tcc atc aag acg gac gtc cac   2512
Ser Tyr Arg Pro Glu Phe Ala Val Gln Ser Ile Lys Thr Asp Val His
            715                 720                 725

agt cct ctt aag tac agg gtg ctg ggc tca cta cag aac ctg cca ggc   2560
Ser Pro Leu Lys Tyr Arg Val Leu Gly Ser Leu Gln Asn Leu Pro Gly
        730                 735                 740

ttc tct gag gca ttc cac tgc cca cga ggc agc ccc atg cac ccc atg   2608
Phe Ser Glu Ala Phe His Cys Pro Arg Gly Ser Pro Met His Pro Met
    745                 750                 755

aag cga tgt cgc atc tgg tagccaaggc tgagctatgc tgcggcccac          2656
Lys Arg Cys Arg Ile Trp
760                 765

gccccgccac ccagaggctt cgcgaatggt gtagctggca gagatgtgca ggtctttgcc 2716

tgaaggccac cggagccacc agccagccct ccgcgcccag cctagagtgt agccacccgc 2776

ccacacccgg gatgagtggt gccggtcctg cgccccctca ggccagtgag ggtcagcagc 2836

ccaggaagag cagtcagctg ccttccaccc tctccatagt gtgtggctaa atgttctcga 2896

gcttcagact tgagctaagt aaacgcttc                                   2925


<210> 13
<211> 765
<212> PRT
<213> Mus musculus

<400> 13
Met Val Glu Arg Ala Gly Trp Cys Arg Lys Lys Ser Pro Gly Phe Val
  1               5                  10                  15

Glu Tyr Gly Leu Met Val Leu Leu Leu Leu Leu Leu Gly Ala Ile Val
```

```
                20                  25                  30

Thr Leu Gly Val Phe Tyr Ser Ile Gly Lys Gln Leu Pro Leu Leu Thr
          35                  40                  45

Ser Leu Leu His Phe Ser Trp Asp Glu Arg Thr Val Val Lys Arg Ala
      50                  55                  60

Leu Arg Asp Ser Ser Leu Lys Ser Asp Ile Cys Thr Thr Pro Ser Cys
 65                  70                  75                  80

Val Ile Ala Ala Ala Arg Ile Leu Glu Asn Met Asp Gln Ser Arg Asn
                 85                  90                  95

Pro Cys Glu Asn Phe Tyr Gln Tyr Ala Cys Gly Gly Trp Leu Arg His
            100                 105                 110

His Val Ile Pro Glu Thr Asn Ser Arg Tyr Ser Val Phe Asp Ile Leu
        115                 120                 125

Arg Asp Glu Leu Glu Val Ile Leu Lys Gly Val Leu Glu Asp Ser Thr
    130                 135                 140

Ser Gln His Arg Pro Ala Val Glu Lys Ala Lys Thr Leu Tyr Arg Ser
145                 150                 155                 160

Cys Met Asn Gln Ser Val Ile Glu Lys Arg Asp Ser Glu Pro Leu Leu
                165                 170                 175

Ser Val Leu Lys Met Val Gly Gly Trp Pro Val Ala Met Asp Lys Trp
            180                 185                 190

Asn Glu Thr Met Gly Leu Lys Trp Glu Leu Glu Arg Gln Leu Ala Val
        195                 200                 205

Leu Asn Ser Gln Phe Asn Arg Arg Val Leu Ile Asp Leu Phe Ile Trp
    210                 215                 220

Asn Asp Asp Gln Asn Ser Ser Arg His Val Ile Tyr Ile Asp Gln Pro
225                 230                 235                 240

Thr Leu Gly Met Pro Ser Arg Glu Tyr Tyr Phe Gln Glu Asp Asn Asn
                245                 250                 255

His Lys Val Arg Lys Ala Tyr Leu Glu Phe Met Thr Ser Val Ala Thr
            260                 265                 270

Met Leu Arg Lys Asp Gln Asn Leu Ser Lys Glu Ser Ala Met Val Arg
        275                 280                 285

Glu Glu Met Ala Glu Val Leu Glu Leu Glu Thr His Leu Ala Asn Ala
    290                 295                 300

Thr Val Pro Gln Glu Lys Arg His Asp Val Thr Ala Leu Tyr His Arg
305                 310                 315                 320

Met Asp Leu Met Glu Leu Gln Glu Arg Phe Gly Leu Lys Gly Phe Asn
```

325 330 335

Trp Thr Leu Phe Ile Gln Asn Val Leu Ser Ser Val Glu Val Glu Leu
340 345 350

Phe Pro Asp Glu Glu Val Val Val Tyr Gly Ile Pro Tyr Leu Glu Asn
355 360 365

Leu Glu Asp Ile Ile Asp Ser Tyr Ser Ala Arg Thr Met Gln Asn Tyr
370 375 380

Leu Val Trp Arg Leu Val Leu Asp Arg Ile Gly Ser Leu Ser Gln Arg
385 390 395 400

Phe Lys Glu Ala Arg Val Asp Tyr Arg Lys Ala Leu Tyr Gly Thr Thr
405 410 415

Val Glu Glu Val Arg Trp Arg Glu Cys Val Ser Tyr Val Asn Ser Asn
420 425 430

Met Glu Ser Ala Val Gly Ser Leu Tyr Ile Lys Arg Ala Phe Ser Lys
435 440 445

Asp Ser Lys Ser Thr Val Arg Glu Leu Ile Glu Lys Ile Arg Ser Val
450 455 460

Phe Val Asp Asn Leu Asp Glu Leu Asn Trp Met Asp Glu Glu Ser Lys
465 470 475 480

Lys Lys Ala Gln Glu Lys Ala Met Asn Ile Arg Glu Gln Ile Gly Tyr
485 490 495

Pro Asp Tyr Ile Leu Glu Asp Asn Asn Lys His Leu Asp Glu Glu Tyr
500 505 510

Ser Ser Leu Thr Phe Tyr Glu Asp Leu Tyr Phe Glu Asn Gly Leu Gln
515 520 525

Asn Leu Lys Asn Asn Ala Gln Arg Ser Leu Lys Lys Leu Arg Glu Lys
530 535 540

Val Asp Gln Asn Leu Trp Ile Ile Gly Ala Ala Val Val Asn Ala Phe
545 550 555 560

Tyr Ser Pro Asn Arg Asn Gln Ile Val Phe Pro Ala Gly Ile Leu Gln
565 570 575

Pro Pro Phe Phe Ser Lys Asp Gln Pro Gln Ser Leu Asn Phe Gly Gly
580 585 590

Ile Gly Met Val Ile Gly His Glu Ile Thr His Gly Phe Asp Asp Asn
595 600 605

Gly Arg Asn Phe Asp Lys Asn Gly Asn Met Leu Asp Trp Trp Ser Asn
610 615 620

Phe Ser Ala Arg His Phe Gln Gln Gln Ser Gln Cys Met Ile Tyr Gln

```
625                 630                 635                 640

Tyr Gly Asn Phe Ser Trp Glu Leu Ala Asp Asn Gln Asn Val Asn Gly
                645                 650                 655

Phe Ser Thr Leu Gly Glu Asn Ile Ala Asp Asn Gly Gly Val Arg Gln
            660                 665                 670

Ala Tyr Lys Ala Tyr Leu Arg Trp Leu Ala Asp Gly Gly Lys Asp Gln
        675                 680                 685

Arg Leu Pro Gly Leu Asn Leu Thr Tyr Ala Gln Leu Phe Phe Ile Asn
    690                 695                 700

Tyr Ala Gln Val Trp Cys Gly Ser Tyr Arg Pro Glu Phe Ala Val Gln
705                 710                 715                 720

Ser Ile Lys Thr Asp Val His Ser Pro Leu Lys Tyr Arg Val Leu Gly
                725                 730                 735

Ser Leu Gln Asn Leu Pro Gly Phe Ser Glu Ala Phe His Cys Pro Arg
            740                 745                 750

Gly Ser Pro Met His Pro Met Lys Arg Cys Arg Ile Trp
        755                 760                 765
```

<210> 14
<211> 2676
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (7)..(2316)

<400> 14

```
gtgggg atg gtg gag agc gcc ggc cgt gca ggg cag aag cgc ccg ggg    48
       Met Val Glu Ser Ala Gly Arg Ala Gly Gln Lys Arg Pro Gly
         1               5                   10

ttc ctg gag ggg ggg ctg ctg ctg ctg ctg ctg ctg gtg acc gct gcc   96
Phe Leu Glu Gly Gly Leu Leu Leu Leu Leu Leu Leu Val Thr Ala Ala
 15                  20                  25                  30

ctg gtg gcc ttg ggt gtc ctc tac gcc gac cgc aga ggg aag cag ctg   144
Leu Val Ala Leu Gly Val Leu Tyr Ala Asp Arg Arg Gly Lys Gln Leu
                35                  40                  45

cca cgc ctt gct agc cgg ctg tgc ttc tta cag gag gag agg acc ttt   192
Pro Arg Leu Ala Ser Arg Leu Cys Phe Leu Gln Glu Glu Arg Thr Phe
            50                  55                  60

gta aaa cga aaa ccc cga ggg atc cca gag gcc caa gag gtg agc gag   240
Val Lys Arg Lys Pro Arg Gly Ile Pro Glu Ala Gln Glu Val Ser Glu
         65                  70                  75
```

```
gtc tgc acc acc cct ggc tgc gtg ata gca gcc gcc agg atc ctc cag   288
Val Cys Thr Thr Pro Gly Cys Val Ile Ala Ala Ala Arg Ile Leu Gln
     80                  85                  90

aac atg gac ccg acc acg gaa ccg tgt gac gac ttc tac cag ttt gca   336
Asn Met Asp Pro Thr Thr Glu Pro Cys Asp Asp Phe Tyr Gln Phe Ala
 95                 100                 105                 110

tgc gga ggc tgg ctg cgg cgc cac gtg atc cct gag acc aac tca aga   384
Cys Gly Gly Trp Leu Arg Arg His Val Ile Pro Glu Thr Asn Ser Arg
                115                 120                 125

tac agc atc ttt gac gtc ctc cgc gac gag ctg gag gtc atc ctc aaa   432
Tyr Ser Ile Phe Asp Val Leu Arg Asp Glu Leu Glu Val Ile Leu Lys
            130                 135                 140

gcg gtg ctg gag aat tcg act gcc aag gac cgg ccg gct gtg gag aag   480
Ala Val Leu Glu Asn Ser Thr Ala Lys Asp Arg Pro Ala Val Glu Lys
        145                 150                 155

gcc agg acg ctg tac cgc tcc tgc atg aac cag agt gtg ata gag aag   528
Ala Arg Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile Glu Lys
    160                 165                 170

cga ggc tct cag ccc ctg ctg gac atc ttg gag gtg gtg gga ggc tgg   576
Arg Gly Ser Gln Pro Leu Leu Asp Ile Leu Glu Val Val Gly Gly Trp
175                 180                 185                 190

ccg gtg gcg atg gac agg tgg aac gag acc gta gga ctc gag tgg gag   624
Pro Val Ala Met Asp Arg Trp Asn Glu Thr Val Gly Leu Glu Trp Glu
                195                 200                 205

ctg gag cgg cag ctg gcg ctg atg aac tca cag ttc aac agg cgc gtc   672
Leu Glu Arg Gln Leu Ala Leu Met Asn Ser Gln Phe Asn Arg Arg Val
            210                 215                 220

ctc atc gac ctc ttc atc tgg aac gac gac cag aac tcc agc cgg cac   720
Leu Ile Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser Arg His
        225                 230                 235

atc atc tac ata gac cag ccc acc ttg ggc atg ccc tcc cga gag tac   768
Ile Ile Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg Glu Tyr
    240                 245                 250

tac ttc aac ggc ggc agc aac cgg aag gtg cgg gaa gcc tac ctg cag   816
Tyr Phe Asn Gly Gly Ser Asn Arg Lys Val Arg Glu Ala Tyr Leu Gln
255                 260                 265                 270

ttc atg gtg tca gtg gcc acg ttg ctg cgg gag gat gca aac ctg ccc   864
Phe Met Val Ser Val Ala Thr Leu Leu Arg Glu Asp Ala Asn Leu Pro
                275                 280                 285

agg gac agc tgc ctg gtg cag gag gac atg gtg cag gtt ctg gag ctg   912
Arg Asp Ser Cys Leu Val Gln Glu Asp Met Val Gln Val Leu Glu Leu
            290                 295                 300
```

```
gag aca cag ctg gcc aag gcc acg gta ccc cag gag gag aga cac gac   960
Glu Thr Gln Leu Ala Lys Ala Thr Val Pro Gln Glu Glu Arg His Asp
        305                 310                 315

gtc atc gcc ttg tac cac cgg atg gga ctg gag gag ctg caa agc cag   1008
Val Ile Ala Leu Tyr His Arg Met Gly Leu Glu Glu Leu Gln Ser Gln
    320                 325                 330

ttt ggc ctg aag gga ttt aac tgg act ctg ttc ata caa act gtg cta   1056
Phe Gly Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Thr Val Leu
335                 340                 345                 350

tcc tct gtc aaa atc aag ctg ctg cca gat gag gaa gtg gtg gtc tat   1104
Ser Ser Val Lys Ile Lys Leu Leu Pro Asp Glu Glu Val Val Val Tyr
                355                 360                 365

ggc atc ccc tac ctg cag aac ctt gaa aac atc atc gac acc tac tca   1152
Gly Ile Pro Tyr Leu Gln Asn Leu Glu Asn Ile Ile Asp Thr Tyr Ser
            370                 375                 380

gcc agg acc ata cag aac tac ctg gtc tgg cgc ctg gtg ctg gac cgc   1200
Ala Arg Thr Ile Gln Asn Tyr Leu Val Trp Arg Leu Val Leu Asp Arg
        385                 390                 395

att ggt agc cta agc cag aga ttc aag gac aca cga gtg aac tac cgc   1248
Ile Gly Ser Leu Ser Gln Arg Phe Lys Asp Thr Arg Val Asn Tyr Arg
    400                 405                 410

aag gcg ctg ttt ggc aca atg gtg gag gag gtg cgc tgg cgt gaa tgt   1296
Lys Ala Leu Phe Gly Thr Met Val Glu Glu Val Arg Trp Arg Glu Cys
415                 420                 425                 430

gtg ggc tac gtc aac agc aac atg gag aac gcc gtg ggc tcc ctc tac   1344
Val Gly Tyr Val Asn Ser Asn Met Glu Asn Ala Val Gly Ser Leu Tyr
                435                 440                 445

gtc agg gag gcg ttc cct gga gac agc aag agc atg gtc aga gaa ctc   1392
Val Arg Glu Ala Phe Pro Gly Asp Ser Lys Ser Met Val Arg Glu Leu
            450                 455                 460

att gac aag gtg cgg aca gtg ttt gtg gag acg ctg gac gag ctg ggc   1440
Ile Asp Lys Val Arg Thr Val Phe Val Glu Thr Leu Asp Glu Leu Gly
        465                 470                 475

tgg atg gac gag gag tcc aag aag aag gcg cag gag aag gcc atg agc   1488
Trp Met Asp Glu Glu Ser Lys Lys Lys Ala Gln Glu Lys Ala Met Ser
    480                 485                 490

atc cgg gag cag atc ggg cac cct gac tac atc ctg gag gag atg aac   1536
Ile Arg Glu Gln Ile Gly His Pro Asp Tyr Ile Leu Glu Glu Met Asn
495                 500                 505                 510

agg cgc ctg gac gag gag tac tcc aat ctg aac ttc tca gag gac ctg   1584
Arg Arg Leu Asp Glu Glu Tyr Ser Asn Leu Asn Phe Ser Glu Asp Leu
                515                 520                 525

tac ttt gag aac agt ctg cag aac ctc aag gtg ggc gcc cag cgg agc   1632
```

```
Tyr Phe Glu Asn Ser Leu Gln Asn Leu Lys Val Gly Ala Gln Arg Ser
            530                 535                 540

ctc agg aag ctt cgg gaa aag gtg gac cca aat ctc tgg atc atc ggg   1680
Leu Arg Lys Leu Arg Glu Lys Val Asp Pro Asn Leu Trp Ile Ile Gly
        545                 550                 555

gcg gcg gtg gtc aat gcg ttc tac tcc cca aac cga aac cag att gta   1728
Ala Ala Val Val Asn Ala Phe Tyr Ser Pro Asn Arg Asn Gln Ile Val
    560                 565                 570

ttc cct gcc ggg atc ctc cag ccc ccc ttc ttc agc aag gag cag cca   1776
Phe Pro Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Lys Glu Gln Pro
575                 580                 585                 590

cag gcc ttg aac ttt gga ggc att ggg atg gtg atc ggg cac gag atc   1824
Gln Ala Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His Glu Ile
                595                 600                 605

acg cac ggc ttt gac gac aat ggc cgg aac ttc gac aag aat ggc aac   1872
Thr His Gly Phe Asp Asp Asn Gly Arg Asn Phe Asp Lys Asn Gly Asn
            610                 615                 620

atg atg gat tgg tgg agt aac ttc tcc acc cag cac ttc cgg gag cag   1920
Met Met Asp Trp Trp Ser Asn Phe Ser Thr Gln His Phe Arg Glu Gln
        625                 630                 635

tca gag tgc atg atc tac cag tac ggc aac tac tcc tgg gac ctg gca   1968
Ser Glu Cys Met Ile Tyr Gln Tyr Gly Asn Tyr Ser Trp Asp Leu Ala
    640                 645                 650

gac gaa cag aac gtg aac gga ttc aac acc ctt ggg gaa aac att gct   2016
Asp Glu Gln Asn Val Asn Gly Phe Asn Thr Leu Gly Glu Asn Ile Ala
655                 660                 665                 670

gac aac gga ggg gtg cgg caa gcc tat aag gcc tac ctc aag tgg atg   2064
Asp Asn Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Lys Trp Met
                675                 680                 685

gca gag ggt ggc aag gac cag cag ctg ccc ggc ctg gat ctc acc cat   2112
Ala Glu Gly Gly Lys Asp Gln Gln Leu Pro Gly Leu Asp Leu Thr His
            690                 695                 700

gag cag ctc ttc ttc atc aac tat gcc cag gtg tgg tgc ggg tcc tac   2160
Glu Gln Leu Phe Phe Ile Asn Tyr Ala Gln Val Trp Cys Gly Ser Tyr
        705                 710                 715

cgg ccc gag ttc gcc atc caa tcc atc aag aca gac gtc cac agt ccc   2208
Arg Pro Glu Phe Ala Ile Gln Ser Ile Lys Thr Asp Val His Ser Pro
    720                 725                 730

ctg aag tac agg gta ctg ggg tcg ctg cag aac ctg gcc gcc ttc gca   2256
Leu Lys Tyr Arg Val Leu Gly Ser Leu Gln Asn Leu Ala Ala Phe Ala
735                 740                 745                 750

gac acg ttc cac tgt gcc cgg ggc acc ccc atg cac ccc aag gag cga   2304
Asp Thr Phe His Cys Ala Arg Gly Thr Pro Met His Pro Lys Glu Arg
```

```
                755                 760                 765

tgc cgc gtg tgg tagccaaggc cctgccgcgc tgtgcggccc acgcccaccc       2356
Cys Arg Val Trp
            770

gctgctcgga ggcatctgtg cgaaggtgca gctagcggcg acccagtgta cgtcccgccc 2416

cggccaacca tgccaagcct gcctgccagg cctctgcgcc tggcctaggg tgcagccacc 2476

tgcctgacac ccagggatga gcagtgtcca gtgcagtacc tggaccggag ccccccttcac 2536

agacacccgc ggggctcagt gcccccgtca caactctgta gagacaatca actgtgtcct 2596

gcccacccct caaggtgcat tgtcttccag tatctacagc ttcagaactt gagctaagta 2656

aatgctttca aagaaaaaaa                                            2676


<210> 15
<211> 770
<212> PRT
<213> Homo sapiens

<400> 15
Met Val Glu Ser Ala Gly Arg Ala Gly Gln Lys Arg Pro Gly Phe Leu
  1               5                  10                  15

Glu Gly Gly Leu Leu Leu Leu Leu Leu Leu Val Thr Ala Ala Leu Val
             20                  25                  30

Ala Leu Gly Val Leu Tyr Ala Asp Arg Arg Gly Lys Gln Leu Pro Arg
         35                  40                  45

Leu Ala Ser Arg Leu Cys Phe Leu Gln Glu Glu Arg Thr Phe Val Lys
     50                  55                  60

Arg Lys Pro Arg Gly Ile Pro Glu Ala Gln Glu Val Ser Glu Val Cys
 65                  70                  75                  80

Thr Thr Pro Gly Cys Val Ile Ala Ala Ala Arg Ile Leu Gln Asn Met
                 85                  90                  95

Asp Pro Thr Thr Glu Pro Cys Asp Asp Phe Tyr Gln Phe Ala Cys Gly
            100                 105                 110

Gly Trp Leu Arg Arg His Val Ile Pro Glu Thr Asn Ser Arg Tyr Ser
        115                 120                 125

Ile Phe Asp Val Leu Arg Asp Glu Leu Glu Val Ile Leu Lys Ala Val
    130                 135                 140

Leu Glu Asn Ser Thr Ala Lys Asp Arg Pro Ala Val Glu Lys Ala Arg
145                 150                 155                 160

Thr Leu Tyr Arg Ser Cys Met Asn Gln Ser Val Ile Glu Lys Arg Gly
                165                 170                 175
```

Ser Gln Pro Leu Leu Asp Ile Leu Glu Val Val Gly Gly Trp Pro Val
180 185 190

Ala Met Asp Arg Trp Asn Glu Thr Val Gly Leu Glu Trp Glu Leu Glu
195 200 205

Arg Gln Leu Ala Leu Met Asn Ser Gln Phe Asn Arg Arg Val Leu Ile
210 215 220

Asp Leu Phe Ile Trp Asn Asp Asp Gln Asn Ser Ser Arg His Ile Ile
225 230 235 240

Tyr Ile Asp Gln Pro Thr Leu Gly Met Pro Ser Arg Glu Tyr Tyr Phe
245 250 255

Asn Gly Gly Ser Asn Arg Lys Val Arg Glu Ala Tyr Leu Gln Phe Met
260 265 270

Val Ser Val Ala Thr Leu Leu Arg Glu Asp Ala Asn Leu Pro Arg Asp
275 280 285

Ser Cys Leu Val Gln Glu Asp Met Val Gln Val Leu Glu Leu Glu Thr
290 295 300

Gln Leu Ala Lys Ala Thr Val Pro Gln Glu Glu Arg His Asp Val Ile
305 310 315 320

Ala Leu Tyr His Arg Met Gly Leu Glu Glu Leu Gln Ser Gln Phe Gly
325 330 335

Leu Lys Gly Phe Asn Trp Thr Leu Phe Ile Gln Thr Val Leu Ser Ser
340 345 350

Val Lys Ile Lys Leu Leu Pro Asp Glu Glu Val Val Val Tyr Gly Ile
355 360 365

Pro Tyr Leu Gln Asn Leu Glu Asn Ile Ile Asp Thr Tyr Ser Ala Arg
370 375 380

Thr Ile Gln Asn Tyr Leu Val Trp Arg Leu Val Leu Asp Arg Ile Gly
385 390 395 400

Ser Leu Ser Gln Arg Phe Lys Asp Thr Arg Val Asn Tyr Arg Lys Ala
405 410 415

Leu Phe Gly Thr Met Val Glu Glu Val Arg Trp Arg Glu Cys Val Gly
420 425 430

Tyr Val Asn Ser Asn Met Glu Asn Ala Val Gly Ser Leu Tyr Val Arg
435 440 445

Glu Ala Phe Pro Gly Asp Ser Lys Ser Met Val Arg Glu Leu Ile Asp
450 455 460

Lys Val Arg Thr Val Phe Val Glu Thr Leu Asp Glu Leu Gly Trp Met
465 470 475 480

Asp Glu Glu Ser Lys Lys Lys Ala Gln Glu Lys Ala Met Ser Ile Arg
485 490 495

Glu Gln Ile Gly His Pro Asp Tyr Ile Leu Glu Glu Met Asn Arg Arg
500 505 510

Leu Asp Glu Glu Tyr Ser Asn Leu Asn Phe Ser Glu Asp Leu Tyr Phe
515 520 525

Glu Asn Ser Leu Gln Asn Leu Lys Val Gly Ala Gln Arg Ser Leu Arg
530 535 540

Lys Leu Arg Glu Lys Val Asp Pro Asn Leu Trp Ile Ile Gly Ala Ala
545 550 555 560

Val Val Asn Ala Phe Tyr Ser Pro Asn Arg Asn Gln Ile Val Phe Pro
565 570 575

Ala Gly Ile Leu Gln Pro Pro Phe Phe Ser Lys Glu Gln Pro Gln Ala
580 585 590

Leu Asn Phe Gly Gly Ile Gly Met Val Ile Gly His Glu Ile Thr His
595 600 605

Gly Phe Asp Asp Asn Gly Arg Asn Phe Asp Lys Asn Gly Asn Met Met
610 615 620

Asp Trp Trp Ser Asn Phe Ser Thr Gln His Phe Arg Glu Gln Ser Glu
625 630 635 640

Cys Met Ile Tyr Gln Tyr Gly Asn Tyr Ser Trp Asp Leu Ala Asp Glu
645 650 655

Gln Asn Val Asn Gly Phe Asn Thr Leu Gly Glu Asn Ile Ala Asp Asn
660 665 670

Gly Gly Val Arg Gln Ala Tyr Lys Ala Tyr Leu Lys Trp Met Ala Glu
675 680 685

Gly Gly Lys Asp Gln Gln Leu Pro Gly Leu Asp Leu Thr His Glu Gln
690 695 700

Leu Phe Phe Ile Asn Tyr Ala Gln Val Trp Cys Gly Ser Tyr Arg Pro
705 710 715 720

Glu Phe Ala Ile Gln Ser Ile Lys Thr Asp Val His Ser Pro Leu Lys
725 730 735

Tyr Arg Val Leu Gly Ser Leu Gln Asn Leu Ala Ala Phe Ala Asp Thr
740 745 750

Phe His Cys Ala Arg Gly Thr Pro Met His Pro Lys Glu Arg Cys Arg
755 760 765

Val Trp
770

<210> 16
<211> 2871
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (205)..(2529)

<400> 16
ggcgctggga gacaccggac gcccgctcgg ctgcgctgcg gctcaggccc ccgctcggcc 60

cgacccgctc ggtcaccgcc ggctcgggcg cgcacctgcc ggctgcggcc ccagggccat 120

gcggaggccc acgaggaggc cggcggccac gcgcatcccg tagcccaggt ggcccaggtc 180

tgcaccgcgg cggcctcggc gccg atg gag ccc ccg tat tcg ctg acg gcg 231
Met Glu Pro Pro Tyr Ser Leu Thr Ala
1 5

cac tac gat gag ttc caa gag gtc aag tac gtg agc cgc tgc ggc gcg 279
His Tyr Asp Glu Phe Gln Glu Val Lys Tyr Val Ser Arg Cys Gly Ala
10 15 20 25

ggg ggc gcg cgc ggg gcc tcc ctg ccc ccg ggc ttc ccg ttg ggc gct 327
Gly Gly Ala Arg Gly Ala Ser Leu Pro Pro Gly Phe Pro Leu Gly Ala
30 35 40

gcg cgc agc gcc acc ggg gcc cgg tcc ggg ctg ccg cgc tgg aac cgg 375
Ala Arg Ser Ala Thr Gly Ala Arg Ser Gly Leu Pro Arg Trp Asn Arg
45 50 55

cgc gag gtg tgc ctg ctg tcg ggg ctg gtg ttc gcc gcc ggc ctc tgc 423
Arg Glu Val Cys Leu Leu Ser Gly Leu Val Phe Ala Ala Gly Leu Cys
60 65 70

gcc att ctg gcg gct atg ctg gcc ctc aag tac ctg ggc ccg gtc gcg 471
Ala Ile Leu Ala Ala Met Leu Ala Leu Lys Tyr Leu Gly Pro Val Ala
75 80 85

gcc ggc ggc ggc gcc tgt ccc gag ggc tgc cct gag cgc aag gcc ttc 519
Ala Gly Gly Gly Ala Cys Pro Glu Gly Cys Pro Glu Arg Lys Ala Phe
90 95 100 105

gcg cgc gcc gct cgc ttc ctg gcc gcc aac ctg gac gcc agc atc gac 567
Ala Arg Ala Ala Arg Phe Leu Ala Ala Asn Leu Asp Ala Ser Ile Asp
110 115 120

cca tgc cag gac ttc tac tcg ttc gcc tgc ggc ggt tgg ctg cgg cgc 615
Pro Cys Gln Asp Phe Tyr Ser Phe Ala Cys Gly Gly Trp Leu Arg Arg
125 130 135

cac gcc atc ccc gac gac aag ctc acc tat ggc acc atc gcg gca atc 663
His Ala Ile Pro Asp Asp Lys Leu Thr Tyr Gly Thr Ile Ala Ala Ile

```
        140                 145                 150

ggc gag caa aac gag gag cgc cta cgg cgc ctg ctg gcg cgg ccc ggg   711
Gly Glu Gln Asn Glu Glu Arg Leu Arg Arg Leu Leu Ala Arg Pro Gly
    155                 160                 165

ggt ggg cct ggc ggc gcg gcc cag cgc aag gtg cgc gcc ttc ttc cgc   759
Gly Gly Pro Gly Gly Ala Ala Gln Arg Lys Val Arg Ala Phe Phe Arg
170                 175                 180                 185

tcg tgc ctc gac atg cgc gag atc gag cga ctg ggc ccg cga ccc atg   807
Ser Cys Leu Asp Met Arg Glu Ile Glu Arg Leu Gly Pro Arg Pro Met
                190                 195                 200

cta gag gtc atc gag gac tgc ggg ggc tgg gac ctg ggc ggc gcg gag   855
Leu Glu Val Ile Glu Asp Cys Gly Gly Trp Asp Leu Gly Gly Ala Glu
            205                 210                 215

gag cgt ccg ggg gtc gcg gcg cga tgg gac ctc aac cgg ctg ctg tac   903
Glu Arg Pro Gly Val Ala Ala Arg Trp Asp Leu Asn Arg Leu Leu Tyr
        220                 225                 230

aag gcg cag ggc gtg tac agc gcc gcc gcg ctc ttc tcg ctc acg gtc   951
Lys Ala Gln Gly Val Tyr Ser Ala Ala Ala Leu Phe Ser Leu Thr Val
    235                 240                 245

agc ctg gac gac agg aac tcc tcg cgc tac gtc atc cgc att gac cag   999
Ser Leu Asp Asp Arg Asn Ser Ser Arg Tyr Val Ile Arg Ile Asp Gln
250                 255                 260                 265

gat ggg ctc acc ctg cca gag agg acc ctg tac ctc gct cag gat gag   1047
Asp Gly Leu Thr Leu Pro Glu Arg Thr Leu Tyr Leu Ala Gln Asp Glu
                270                 275                 280

gac agt gag aag gtc ctg gca gca tac agg gtg ttc atg gag cga gtg   1095
Asp Ser Glu Lys Val Leu Ala Ala Tyr Arg Val Phe Met Glu Arg Val
            285                 290                 295

ctc agc ctc ctg ggt gca gac gct gtg gaa cag aag gcc caa gag atc   1143
Leu Ser Leu Leu Gly Ala Asp Ala Val Glu Gln Lys Ala Gln Glu Ile
        300                 305                 310

ctg caa gtg gag cag cag ctg gcc aac atc act gtg tca gag tat gac   1191
Leu Gln Val Glu Gln Gln Leu Ala Asn Ile Thr Val Ser Glu Tyr Asp
    315                 320                 325

gac cta cgg cga gat gtc agc tcc atg tac aac aag gtg acg ctg ggg   1239
Asp Leu Arg Arg Asp Val Ser Ser Met Tyr Asn Lys Val Thr Leu Gly
330                 335                 340                 345

cag ctg cag aag atc acc ccc cac ttg cgg tgg aag tgg ctg cta gac   1287
Gln Leu Gln Lys Ile Thr Pro His Leu Arg Trp Lys Trp Leu Leu Asp
                350                 355                 360

cag atc ttc cag gag gac ttc tca gag gaa gag gag gtg gtg ctg ctg   1335
Gln Ile Phe Gln Glu Asp Phe Ser Glu Glu Glu Glu Val Val Leu Leu
            365                 370                 375
```

```
gcg aca gac tac atg cag cag gtg tcg cag ctc atc cgc tcc aca ccc   1383
Ala Thr Asp Tyr Met Gln Gln Val Ser Gln Leu Ile Arg Ser Thr Pro
        380                 385                 390

cac cgg gtc ctg cac aac tac ctg gtg tgg cgc gtg gtg gtg gtc ctg   1431
His Arg Val Leu His Asn Tyr Leu Val Trp Arg Val Val Val Val Leu
    395                 400                 405

agt gaa cac ctg tcc ccg cca ttc cgt gag gca ctg cac gag ctg gca   1479
Ser Glu His Leu Ser Pro Pro Phe Arg Glu Ala Leu His Glu Leu Ala
410                 415                 420                 425

cag gag atg gag ggc agc gac aag cca cag gag ctg gcc cgg gtc tgc   1527
Gln Glu Met Glu Gly Ser Asp Lys Pro Gln Glu Leu Ala Arg Val Cys
                430                 435                 440

ttg ggc cag gcc aat cgc cac ttt ggc atg gcg ctt ggc gcc ctc ttt   1575
Leu Gly Gln Ala Asn Arg His Phe Gly Met Ala Leu Gly Ala Leu Phe
            445                 450                 455

gta cat gag cac ttc tca gct gcc agc aaa gcc aag gtg cag cag cta   1623
Val His Glu His Phe Ser Ala Ala Ser Lys Ala Lys Val Gln Gln Leu
        460                 465                 470

gtg gaa gac atc aag tac atc ctg ggc cag cgc ctg gag gag ctg gac   1671
Val Glu Asp Ile Lys Tyr Ile Leu Gly Gln Arg Leu Glu Glu Leu Asp
    475                 480                 485

tgg atg gac gcc gag acc agg gct gct gct cgg gcc aag ctc cag tac   1719
Trp Met Asp Ala Glu Thr Arg Ala Ala Ala Arg Ala Lys Leu Gln Tyr
490                 495                 500                 505

atg atg gtg atg gtc ggc tac ccg gac ttc ctg ctg aaa ccc gat gct   1767
Met Met Val Met Val Gly Tyr Pro Asp Phe Leu Leu Lys Pro Asp Ala
                510                 515                 520

gtg gac aag gag tat gag ttt gag gtc cat gag aag acc tac ttc aag   1815
Val Asp Lys Glu Tyr Glu Phe Glu Val His Glu Lys Thr Tyr Phe Lys
            525                 530                 535

aac atc ttg aac agc atc cgc ttc agc atc cag ctc tca gtt aag aag   1863
Asn Ile Leu Asn Ser Ile Arg Phe Ser Ile Gln Leu Ser Val Lys Lys
        540                 545                 550

att cgg cag gag gtg gac aag tcc acg tgg ctg ctc ccc cca cag gcg   1911
Ile Arg Gln Glu Val Asp Lys Ser Thr Trp Leu Leu Pro Pro Gln Ala
    555                 560                 565

ctc aat gcc tac tat cta ccc aac aag aac cag atg gtg ttc ccc gcg   1959
Leu Asn Ala Tyr Tyr Leu Pro Asn Lys Asn Gln Met Val Phe Pro Ala
570                 575                 580                 585

ggc atc ctg cag ccc acc ctg tac gac cct gac ttc cca cag tct ctc   2007
Gly Ile Leu Gln Pro Thr Leu Tyr Asp Pro Asp Phe Pro Gln Ser Leu
                590                 595                 600
```

```
aac tac ggg ggc atc ggc acc atc att gga cat gag ctg acc cac ggc   2055
Asn Tyr Gly Gly Ile Gly Thr Ile Ile Gly His Glu Leu Thr His Gly
            605                 610                 615

tac gac gac tgg ggg ggc cag tat gac cgc tca ggg aac ctg ctg cac   2103
Tyr Asp Asp Trp Gly Gly Gln Tyr Asp Arg Ser Gly Asn Leu Leu His
        620                 625                 630

tgg tgg acg gag gcc tcc tac agc cgc ttc ctg cga aag gct gag tgc   2151
Trp Trp Thr Glu Ala Ser Tyr Ser Arg Phe Leu Arg Lys Ala Glu Cys
    635                 640                 645

atc gtc cgt ctc tat gac aac ttc act gtc tac aac cag cgg gtg aac   2199
Ile Val Arg Leu Tyr Asp Asn Phe Thr Val Tyr Asn Gln Arg Val Asn
650                 655                 660                 665

ggg aaa cac acg ctt ggg gag aac atc gca gat atg ggc ggc ctc aag   2247
Gly Lys His Thr Leu Gly Glu Asn Ile Ala Asp Met Gly Gly Leu Lys
                670                 675                 680

ctg gcc tac cac gcc tat cag aag tgg gtg cgg gag cac ggc cca gag   2295
Leu Ala Tyr His Ala Tyr Gln Lys Trp Val Arg Glu His Gly Pro Glu
            685                 690                 695

cac cca ctt ccc cgg ctc aag tac aca cat gac cag ctc ttc ttc att   2343
His Pro Leu Pro Arg Leu Lys Tyr Thr His Asp Gln Leu Phe Phe Ile
        700                 705                 710

gcc ttt gcc cag aac tgg tgc atc aag cgg cgg tcg cag tcc atc tac   2391
Ala Phe Ala Gln Asn Trp Cys Ile Lys Arg Arg Ser Gln Ser Ile Tyr
    715                 720                 725

ctg cag gtg ctg act gac aag cat gcc cct gag cac tac agg gtg ctg   2439
Leu Gln Val Leu Thr Asp Lys His Ala Pro Glu His Tyr Arg Val Leu
730                 735                 740                 745

ggc agt gtg tcc cag ttt gag gag ttt ggc cgg gtt tta cac tgt cca   2487
Gly Ser Val Ser Gln Phe Glu Glu Phe Gly Arg Val Leu His Cys Pro
                750                 755                 760

aag gtc tca ccc atg aac cct gcc cac aag tgt tcc gtg tgg           2529
Lys Val Ser Pro Met Asn Pro Ala His Lys Cys Ser Val Trp
            765                 770                 775

tgaccctggc tgcccgcctg cacgccccca ctgcccccgc acgaatcacc tcctgctggc 2589

taccggggca ggcatgcacc cggtgccagc cccgctctgg gcaccacctg ccttccagcc 2649

cctccaggac ccggtccccc tgctgcccct cacttcagga ggggcctgga gcagggtgag 2709

gctggacttt ggggggctgt gagggaaata tactggggtc cccagattct gctctaaggg 2769

ggccagaccc tctgccaggc tggattgtac gggccccacc ttcgctgtgt tcttgctgca 2829

agtctggtca aataaatcac tgcactgtta aaaaaaaaaa aa                     2871
```

<210> 17
<211> 775
<212> PRT
<213> Homo sapiens

<400> 17

```
Met Glu Pro Pro Tyr Ser Leu Thr Ala His Tyr Asp Glu Phe Gln Glu
  1               5                  10                  15

Val Lys Tyr Val Ser Arg Cys Gly Ala Gly Gly Ala Arg Gly Ala Ser
             20                  25                  30

Leu Pro Pro Gly Phe Pro Leu Gly Ala Ala Arg Ser Ala Thr Gly Ala
         35                  40                  45

Arg Ser Gly Leu Pro Arg Trp Asn Arg Arg Glu Val Cys Leu Leu Ser
     50                  55                  60

Gly Leu Val Phe Ala Ala Gly Leu Cys Ala Ile Leu Ala Ala Met Leu
 65                  70                  75                  80

Ala Leu Lys Tyr Leu Gly Pro Val Ala Ala Gly Gly Gly Ala Cys Pro
                 85                  90                  95

Glu Gly Cys Pro Glu Arg Lys Ala Phe Ala Arg Ala Ala Arg Phe Leu
            100                 105                 110

Ala Ala Asn Leu Asp Ala Ser Ile Asp Pro Cys Gln Asp Phe Tyr Ser
        115                 120                 125

Phe Ala Cys Gly Gly Trp Leu Arg Arg His Ala Ile Pro Asp Asp Lys
    130                 135                 140

Leu Thr Tyr Gly Thr Ile Ala Ala Ile Gly Glu Gln Asn Glu Glu Arg
145                 150                 155                 160

Leu Arg Arg Leu Leu Ala Arg Pro Gly Gly Gly Pro Gly Gly Ala Ala
                165                 170                 175

Gln Arg Lys Val Arg Ala Phe Phe Arg Ser Cys Leu Asp Met Arg Glu
            180                 185                 190

Ile Glu Arg Leu Gly Pro Arg Pro Met Leu Glu Val Ile Glu Asp Cys
        195                 200                 205

Gly Gly Trp Asp Leu Gly Gly Ala Glu Glu Arg Pro Gly Val Ala Ala
    210                 215                 220

Arg Trp Asp Leu Asn Arg Leu Leu Tyr Lys Ala Gln Gly Val Tyr Ser
225                 230                 235                 240

Ala Ala Ala Leu Phe Ser Leu Thr Val Ser Leu Asp Asp Arg Asn Ser
                245                 250                 255

Ser Arg Tyr Val Ile Arg Ile Asp Gln Asp Gly Leu Thr Leu Pro Glu
            260                 265                 270
```

```
Arg Thr Leu Tyr Leu Ala Gln Asp Glu Asp Ser Glu Lys Val Leu Ala
        275                 280                 285

Ala Tyr Arg Val Phe Met Glu Arg Val Leu Ser Leu Leu Gly Ala Asp
    290                 295                 300

Ala Val Glu Gln Lys Ala Gln Glu Ile Leu Gln Val Glu Gln Gln Leu
305                 310                 315                 320

Ala Asn Ile Thr Val Ser Glu Tyr Asp Asp Leu Arg Arg Asp Val Ser
                325                 330                 335

Ser Met Tyr Asn Lys Val Thr Leu Gly Gln Leu Gln Lys Ile Thr Pro
            340                 345                 350

His Leu Arg Trp Lys Trp Leu Leu Asp Gln Ile Phe Gln Glu Asp Phe
        355                 360                 365

Ser Glu Glu Glu Glu Val Val Leu Leu Ala Thr Asp Tyr Met Gln Gln
    370                 375                 380

Val Ser Gln Leu Ile Arg Ser Thr Pro His Arg Val Leu His Asn Tyr
385                 390                 395                 400

Leu Val Trp Arg Val Val Val Val Leu Ser Glu His Leu Ser Pro Pro
                405                 410                 415

Phe Arg Glu Ala Leu His Glu Leu Ala Gln Glu Met Glu Gly Ser Asp
            420                 425                 430

Lys Pro Gln Glu Leu Ala Arg Val Cys Leu Gly Gln Ala Asn Arg His
        435                 440                 445

Phe Gly Met Ala Leu Gly Ala Leu Phe Val His Glu His Phe Ser Ala
    450                 455                 460

Ala Ser Lys Ala Lys Val Gln Gln Leu Val Glu Asp Ile Lys Tyr Ile
465                 470                 475                 480

Leu Gly Gln Arg Leu Glu Glu Leu Asp Trp Met Asp Ala Glu Thr Arg
                485                 490                 495

Ala Ala Ala Arg Ala Lys Leu Gln Tyr Met Met Val Met Val Gly Tyr
            500                 505                 510

Pro Asp Phe Leu Leu Lys Pro Asp Ala Val Asp Lys Glu Tyr Glu Phe
        515                 520                 525

Glu Val His Glu Lys Thr Tyr Phe Lys Asn Ile Leu Asn Ser Ile Arg
    530                 535                 540

Phe Ser Ile Gln Leu Ser Val Lys Lys Ile Arg Gln Glu Val Asp Lys
545                 550                 555                 560

Ser Thr Trp Leu Leu Pro Pro Gln Ala Leu Asn Ala Tyr Tyr Leu Pro
                565                 570                 575
```

```
Asn Lys Asn Gln Met Val Phe Pro Ala Gly Ile Leu Gln Pro Thr Leu
            580                 585                 590

Tyr Asp Pro Asp Phe Pro Gln Ser Leu Asn Tyr Gly Gly Ile Gly Thr
        595                 600                 605

Ile Ile Gly His Glu Leu Thr His Gly Tyr Asp Asp Trp Gly Gly Gln
    610                 615                 620

Tyr Asp Arg Ser Gly Asn Leu Leu His Trp Trp Thr Glu Ala Ser Tyr
625                 630                 635                 640

Ser Arg Phe Leu Arg Lys Ala Glu Cys Ile Val Arg Leu Tyr Asp Asn
                645                 650                 655

Phe Thr Val Tyr Asn Gln Arg Val Asn Gly Lys His Thr Leu Gly Glu
            660                 665                 670

Asn Ile Ala Asp Met Gly Gly Leu Lys Leu Ala Tyr His Ala Tyr Gln
        675                 680                 685

Lys Trp Val Arg Glu His Gly Pro Glu His Pro Leu Pro Arg Leu Lys
    690                 695                 700

Tyr Thr His Asp Gln Leu Phe Phe Ile Ala Phe Ala Gln Asn Trp Cys
705                 710                 715                 720

Ile Lys Arg Arg Ser Gln Ser Ile Tyr Leu Gln Val Leu Thr Asp Lys
                725                 730                 735

His Ala Pro Glu His Tyr Arg Val Leu Gly Ser Val Ser Gln Phe Glu
            740                 745                 750

Glu Phe Gly Arg Val Leu His Cys Pro Lys Val Ser Pro Met Asn Pro
        755                 760                 765

Ala His Lys Cys Ser Val Trp
    770                 775
```